Draft

This Raw Listing contains the General Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Wild, Hanno; Hanko, Rudolf; Dorschug, Michael; Horlein, Hans-Dietrich; Beunink, Jurgen; Apeler, Heiner; Wehlmann, Hermann; and Sebald, Walter

(ii) TITLE OF INVENTION: HIL-4 MUTANT PROTEINS USED AS ANTAGONISTS OR PARTIAL AGONISTS OF HUMAN INTERLEUKIN 4

(iii) NUMBER OF SEQUENCES: 20

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Sprung Kramer Schaefer & Briscoe

(B) STREET: 660 White Plains Road

(C) CITY: Tarrytown

(D) STATE: New York

(E) COUNTRY: USA

(F) ZIP: 10591-5144

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage

(B) COMPUTER: Apple Macintosh

(C) OPERATING SYSTEM: System 7.5

(D) SOFTWARE: WordPerfect 3.5

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/765,012

(B) FILING DATE: 19-DEC-1996

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/EP95/02358

(B) FILING DATE: 19-JUN-1995

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: DE 44 23 131

(B) FILING DATE: 01-JUL-1994

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kurt G. Briscoe

(B) REGISTRATION NUMBER: 33,141

(C) REFERENCE/DOCKET NUMBER: BAYER 9776-KGB

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (914) 332-1700

(B) TELEFAX: (914) 332-1844

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: synthetic
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CATGCACAAG TGCGAT 16

(2) INFORMATION FOR SEQ ID NO: 2:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: synthetic
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATCGCACTTG TG 12

(2) INFORMATION FOR SEQ ID NO: 3:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: synthetic
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCCTCCAAGG ACACAACTGA G 21

(2) INFORMATION FOR SEQ ID NO: 4:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: synthetic

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GTGAAGGAAG CCGACCAGAG TACG 24

(2) INFORMATION FOR SEQ ID NO: 5:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: synthetic
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTGGAGACTG CCATGGCCCA CAAGTGCGAT ATCACC 36

(2) INFORMATION FOR SEQ ID NO: 6:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Ala His Lys Cys Asp Ile Thr Leu Gln Glu
1 5

Ile Ile Lys Thr Leu Asn Ser Leu Thr Glu
10 15

Gln Lys Thr Leu Cys Thr Glu Leu Thr Val
20 25

Thr Asp Ile Phe Ala Ala Ser Lys Asn Thr
30 35

Thr Glu Asn Glu Thr Phe Cys Arg Ala Ala
40 45

Thr Val Leu Arg Gln Phe Tyr Ser His His
50 55

Glu Lys Asp Thr Arg Cys Leu Gly Ala Thr
60 65

Ala Gln Gln Phe His Arg His Lys Gln Leu
70 75

Ile Arg Phe Leu Lys Arg Leu Asp Arg Asn

153 80 85
154
155 Leu Trp Gly Leu Ala Gly Leu Asn Ser Cys
156 90 95
157
158 Pro Val Lys Glu Ala Asn Gln Ser Thr Leu
159 100 105
160
161 Glu Asn Phe Leu Glu Arg Leu Lys Thr Ile
162 110 115
163
164 Met Arg Glu Lys Asp Ser Lys Cys Ser Ser
165 120 125
166
167
168 (2) INFORMATION FOR SEQ ID NO: 7:
169 (i) SEQUENCE CHARACTERISTICS:
170 (A) LENGTH: 131 amino acids
171 (B) TYPE: amino acid
172 (D) TOPOLOGY: linear
173 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
174
175
176 Met Ala His Lys Cys Asp Ile Thr Leu Gln Glu
177 1 5
178
179 Ile Ile Lys Thr Leu Asn Ser Leu Thr Glu
180 10 15
181
182 Gln Lys Thr Leu Cys Thr Glu Leu Thr Val
183 20 25
184
185 Thr Asp Ile Phe Ala Ala Ser Lys Asn Thr
186 30 35
187
188 Thr Glu Asn Glu Thr Phe Cys Arg Ala Ala
189 40 45
190
191 Thr Val Leu Arg Gln Phe Tyr Ser His His
192 50 55
193
194 Glu Lys Asp Thr Arg Cys Leu Gly Ala Thr
195 60 65
196
197 Ala Gln Gln Phe His Arg His Lys Gln Leu
198 70 75
199
200 Ile Arg Phe Leu Lys Arg Leu Asp Arg Asn
201 80 85
202
203 Leu Trp Gly Leu Ala Gly Leu Asn Ser Cys
204 90 95
205

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Pro Val Lys Glu Ala Asn Gln Ser Thr Leu
100                 105

Glu Asn Phe Leu Glu Arg Leu Lys Thr Ile
110                 115

Met Asp Glu Lys Asp Ser Lys Cys Ser Ser
120                 125


(2) INFORMATION FOR SEQ ID NO: 8:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 8:


Met Ala His Lys Cys Asp Ile Thr Leu Gln Glu
          1               5

Ile Ile Lys Thr Leu Asn Ser Leu Thr Glu
 10                  15

Gln Lys Thr Leu Cys Thr Glu Leu Thr Val
 20                  25

Thr Asp Ile Phe Ala Ala Ser Lys Asn Thr
 30                  35

Thr Glu Asn Glu Thr Phe Cys Arg Ala Ala
 40                  45

Thr Val Leu Arg Gln Phe Tyr Ser His His
 50                  55

Glu Lys Asp Thr Arg Cys Leu Gly Ala Thr
 60                  65

Ala Gln Gln Phe His Arg His Lys Gln Leu
 70                  75

Ile Arg Phe Leu Lys Arg Leu Asp Arg Asn
 80                  85

Leu Trp Gly Leu Ala Gly Leu Asn Ser Cys
 90                  95

Pro Val Lys Glu Ala Asn Gln Ser Thr Leu
100                 105

Glu Asn Phe Leu Glu Arg Leu Lys Thr Ile
110                 115
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SEQUENCE VERIFICATION REPORT
.PATENT APPLICATION *US/08/765,012A*

DATE: 09/15/98
TIME: 15:22:09

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